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12.   (Once Amended) The method of claim 1, wherein said second process is executed using a <u>sequence comparison algorithm</u> [BLAST algorithm].

27.   (Once Amended) The method of claim 18, wherein the identification of repeat sequences within said genomic region is performed using [Repeat Masker software] <u>a software program that screens sequences for:</u>

    i.   <u>interspersed repeats that are known to exist in mammalian genomes and:</u>

    ii.   <u>low complexity DNA sequences</u>.

28.   (Once Amended) The method of claim 18, wherein the comparison of said at least one repeat sequence-free subsequence with said genome database is performed using a <u>sequence comparison algorithm</u> [BLAST algorithm].

40.   (New) The method of claim 1, wherein the repeat-free subsequences are each at least 100 bp long.

41.   (New) The method of claim 18, wherein the repeat-free subsequences are each at least 100 bp long.

42.   (New) The computer program of claim 34, wherein each nucleotide sequence that does not contain any of the repeat sequences is at least 100 bp long.

<div align="center">REMARKS</div>

I.   ***Status of the Claims***

Claims 11-12 and 27-28 are amended and claims 40-42 are added with this Amendment. Claim 39 is canceled without prejudice to further prosecution. Therefore, claims 1-38 and 40-42 are pending with entry of this Amendment. Appendix A contains a marked-up copy of the amendments. For the convenience of the Examiner, Appendix B provides a list of all claims pending with entry of this Amendment.